1600

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/660,302C

DATE: 07/31/2002 P·6
TIME: 10:05:17

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\07312002\I660302C.raw**

```
 1 <110> APPLICANT: Universiteit Utrecht
 2       Strous, Gerardus
 3       Van Kerkhof, Petrus
 4       Govers, Roland
 6 <120> TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF
PROTEASE
 7       INHIBITORS OR RECEPTOR FRAGMENTS
 9 <130> FILE REFERENCE: 2183-4525US
 11 <140> CURRENT APPLICATION NUMBER: US/09/660,302C
 12 <141> CURRENT FILING DATE: 2000-09-12
 14 <150> PRIOR APPLICATION NUMBER: PCT/NL99/00136
 15 <151> PRIOR FILING DATE: 1999-03-12
 17 <150> PRIOR APPLICATION NUMBER: EP98200799.9
 18 <151> PRIOR FILING DATE: 1998-03-12
 20 <160> NUMBER OF SEQ ID NOS: 50
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 8
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Unknown
 29 <220> FEATURE:
 30 <221> NAME/KEY: BINDING
 31 <222> LOCATION: (1)..(8)
 32 <223> OTHER INFORMATION: synthetic peptide, Binding polypeptide motif
 34 <220> FEATURE:
 35 <221> NAME/KEY: UNSURE
 36 <222> LOCATION: (1)..(1)
 37 <223> OTHER INFORMATION: Xaa may be any amino acid
 39 <220> FEATURE:
 40 <221> NAME/KEY: UNSURE
 41 <222> LOCATION: (2)..(2)
 42 <223> OTHER INFORMATION: Xaa is E, but may be replaced by D
 44 <220> FEATURE:
 45 <221> NAME/KEY: UNSURE
 46 <222> LOCATION: (3)..(3)
 47 <223> OTHER INFORMATION: Xaa is F, but may be replaced by Y
 49 <220> FEATURE:
 50 <221> NAME/KEY: UNSURE
 51 <222> LOCATION: (4)..(4)
 52 <223> OTHER INFORMATION: Xaa is I, but may be replaced by L, V or F
 54 <220> FEATURE:
 55 <221> NAME/KEY: UNSURE
 56 <222> LOCATION: (5)..(5)
 57 <223> OTHER INFORMATION: Xaa may be any amino acid
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C--> 11 **<140> CURRENT APPLICATION NUMBER: US/09/660,302C**

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     59 <220> FEATURE:
     60 <221> NAME/KEY: UNSURE
     61 <222> LOCATION: (6)..(6)
     62 <223> OTHER INFORMATION: Xaa may be any amino acid
     64 <220> FEATURE:
     65 <221> NAME/KEY: UNSURE
     66 <222> LOCATION: (7)..(7)
     67 <223> OTHER INFORMATION: Xaa is D, but may be replaced by E
     69 <220> FEATURE:
     70 <221> NAME/KEY: UNSURE
     71 <222> LOCATION: (8)..(8)
     72 <223> OTHER INFORMATION: Xaa may be any amino acid
     74 <400> SEQUENCE: 1
W--> 75 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     76 1               5
     78 <210> SEQ ID NO: 2
     79 <211> LENGTH: 12
     80 <212> TYPE: PRT
     81 <213> ORGANISM: Unknown
     83 <220> FEATURE:
     84 <223> OTHER INFORMATION: Unsure, Growth hormone receptor binding motif, Binds to
hormone receptor
     85       and ubiquitin
     87 <400> SEQUENCE: 2
     88 Asp Asp Ser Trp Val Glu Phe Ile Glu Leu Asp Ile
     89 1               5                   10
     91 <210> SEQ ID NO: 3
     92 <211> LENGTH: 10
     93 <212> TYPE: PRT
     94 <213> ORGANISM: Unknown
     96 <220> FEATURE:
     97 <223> OTHER INFORMATION: Unsure, Growth hormone receptor motif, Binds to hormone
receptor and
     98       ubiquitin
    100 <400> SEQUENCE: 3
    101 Asp Ser Trp Val Glu Phe Ile Glu Leu Asp
    102 1               5                   10
    104 <210> SEQ ID NO: 4
    105 <211> LENGTH: 129
    106 <212> TYPE: PRT
    107 <213> ORGANISM: Unknown
    109 <220> FEATURE:
    110 <223> OTHER INFORMATION: Unsure, Growth hormone receptor motif, Up-regulates GH
activity
    112 <400> SEQUENCE: 4
    113 Ser Lys Gln Gln Arg Ile Lys Met Leu Ile Leu Pro Pro Val Pro Val
    114 1               5                   10                  15
    115 Pro Lys Ile Lys Gly Ile Asp Pro Asp Leu Leu Lys Glu Gly Lys Leu
    116             20                  25                  30
    117 Glu Glu Val Asn Thr Ile Leu Ala Ile His Asp Ser Tyr Lys Pro Glu
    118             35                  40                  45
    119 Phe His Ser Asp Asp Ser Trp Val Glu Phe Ile Glu Leu Asp Ile Asp
```

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```
120     50                  55                 60
121 Glu Pro Asp Glu Lys Thr Glu Glu Ser Asp Thr Asp Leu Leu Ser Ser
122 65                  70                 75                 80
123 Asp His Glu Lys Ser His Ser Asn Leu Gly Val Lys Asp Gly Asp Ser
124                 85                 90                 95
125 Gly Arg Thr Ser Cys Cys Glu Pro Asp Ile Leu Glu Thr Asp Phe Asn
126                 100                105                110
127 Ala Asn Asp Ile His Glu Gly Thr Ser Glu Val Ala Gln Pro Gln Arg
128         115                120                125  .
129 Leu
131 <210> SEQ ID NO: 5
132 <211> LENGTH: 38
133 <212> TYPE: PRT
134 <213> ORGANISM: Unknown
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Unsure, Derived from protein receptor, Up-regulates GH
activity
139 <400> SEQUENCE: 5
140 Lys Asp Gly Asp Ser Gly Arg Thr Ser Cys Cys Glu Pro Asp Ile Leu
141 1           5                  10                 15
142 Glu Thr Asp Phe Asn Ala Asn Phe Ile His Glu Gly Thr Ser Glu Val
143                 20                 25                 30
144 Ala Gln Pro Gln Arg Leu
145         35
147 <210> SEQ ID NO: 6
148 <211> LENGTH: 10
149 <212> TYPE: PRT
150 <213> ORGANISM: Unknown
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Unsure, Glut4 Ins-regulated glucose transporter binding
motif, Binds to
154         ubiquitin/proteasome system binding site
156 <400> SEQUENCE: 6
157 Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu
158 1           5                  10
160 <210> SEQ ID NO: 7
161 <211> LENGTH: 7
162 <212> TYPE: PRT
163 <213> ORGANISM: Unknown
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Unsure, Binding poly-peptide motif, Binds to
ubiquitin/proteasome system
167         binding site
169 <400> SEQUENCE: 7
170 Cys Glu Glu Asp Phe Tyr Arg
171 1               5
173 <210> SEQ ID NO: 8
174 <211> LENGTH: 10
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens (human) or Lepus unknown species (rabbit)
178 <220> FEATURE:
179 <223> OTHER INFORMATION: GHR sequence
```

RAW SEQUENCE LISTING   DATE: 07/31/2002
PATENT APPLICATION: US/09/660,302C TIME: 10:05:17

Input Set : **A:\EP.txt**
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```
181 <400> SEQUENCE: 8
182 Ser Trp Val Glu Phe Ile Glu Leu Asp Ile
183 1               5               10
185 <210> SEQ ID NO: 9
186 <211> LENGTH: 10
187 <212> TYPE: PRT
188 <213> ORGANISM: Gallus gallus (chicken)
190 <220> FEATURE:
191 <223> OTHER INFORMATION: GHR
193 <400> SEQUENCE: 9
194 Leu Trp Val Glu Phe Ile Glu Leu Asp Ile
195 1               5               10
197 <210> SEQ ID NO: 10
198 <211> LENGTH: 10
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens (human)
202 <220> FEATURE:
203 <223> OTHER INFORMATION: prolactin receptor
205 <400> SEQUENCE: 10
206 Leu Leu Val Glu Tyr Leu Glu Val Asp Asp
207 1               5               10
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 10
211 <212> TYPE: PRT
212 <213> ORGANISM: Mus musculus (mouse), Lepus unknown species (rabbit), or Rattus
unknown
W--> 213 species (rat)
215 <220> FEATURE:
216 <223> OTHER INFORMATION: prolactin receptor
218 <400> SEQUENCE: 11
219 Leu Leu Val Glu Phe Leu Glu Asn Asp Asp
220 1               5               10
222 <210> SEQ ID NO: 12
223 <211> LENGTH: 10
224 <212> TYPE: PRT
225 <213> ORGANISM: Unknown
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Unsure, vertebrate skeletal muscle
230 <400> SEQUENCE: 12
231 Asp Asn Val Asp Tyr Leu Thr Arg Asp Trp
232 1               5               10
234 <210> SEQ ID NO: 13
235 <211> LENGTH: 10
236 <212> TYPE: PRT
237 <213> ORGANISM: Unknown
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Unsure, FGF Receptor Family
242 <400> SEQUENCE: 13
243 Gln Ala Ala Glu Tyr Leu Arg Ser Glu Thr
244 1               5               10
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PATENT APPLICATION: US/09/660,302C   TIME: 10:05:17

Input Set : A:\EP.txt
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246 <210> SEQ ID NO: 14
247 <211> LENGTH: 10
248 <212> TYPE: PRT
249 <213> ORGANISM: Unknown
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Unsure, Transmembrane receptor sex precursor
254 <400> SEQUENCE: 14
255 Ile Asp Ala Glu Tyr Ile Ser Ala Glu Arg
256 1               5                   10
258 <210> SEQ ID NO: 15
259 <211> LENGTH: 10
260 <212> TYPE: PRT
261 <213> ORGANISM: Unknown
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Unsure, IgE Receptor
266 <400> SEQUENCE: 15
267 Leu Lys Gly Glu Phe Ile Trp Val Asp Gly
268 1               5                   10
270 <210> SEQ ID NO: 16
271 <211> LENGTH: 10
272 <212> TYPE: PRT
273 <213> ORGANISM: Unknown
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Unsure, ANGIOTENSIN CONVERTING ENZYME
278 <400> SEQUENCE: 16
279 Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly
280 1               5                   10
282 <210> SEQ ID NO: 17
283 <211> LENGTH: 10
284 <212> TYPE: PRT
285 <213> ORGANISM: Unknown
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Unsure, POTASSIUM CHANNEL IRK
290 <400> SEQUENCE: 17
291 Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln
292 1               5                   10
294 <210> SEQ ID NO: 18
295 <211> LENGTH: 10
296 <212> TYPE: PRT
297 <213> ORGANISM: Unknown
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Unsure, PDGF RECEPTOR ALPHA-CHAIN
302 <400> SEQUENCE: 18
303 Asp Gly His Glu Tyr Ile Tyr Val Asp Pro
304 1               5                   10
306 <210> SEQ ID NO: 19
307 <211> LENGTH: 10
308 <212> TYPE: PRT
309 <213> ORGANISM: Unknown
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/31/2002
PATENT APPLICATION: US/09/660,302C   TIME: 10:05:18

Input Set : **A:\EP.txt**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,3,4,5,6,7,8
Seq#:50; Xaa Pos. 4

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 84
Seq#:7; Line(s) 166

VERIFICATION SUMMARY   DATE: 07/31/2002
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:213 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:322 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0